by the pathogen to inhibit a biological function within said pathogen, wherein said polynucleotide sequence exhibits from about 95 to about 100% nucleotide sequence identity along at least from about 19 to about 25 contiguous nucleotides to a coding sequence derived from said pathogen or its host plant and is hybridized to a second polynucleotide sequence that is complementary to said first polynucleotide sequence, and wherein said coding sequence derived from said pathogen or host is selected from the group consisting of SEQ ID NOs:3-15; SEQ ID NOs:18-23, SEQ ID NO:29, or SEQ ID NO:s:33-35 and the complements thereof.

19. The method of claim **18**, wherein said pathogen is an ascomycete, a basidiomycete, a deuteromycete, or an oomycete.

20. A method for controlling a fungal or oomycete plant disease comprising providing in the host plant of a fungal or oomycete plant pathogen a transformed plant cell expressing a polynucleotide sequence according to claim **1**, wherein the polynucleotide is expressed to produce a double stranded ribonucleic acid that functions upon being taken up by the pathogen to inhibit the expression of a target sequence within said pathogen and results in decreased growth, in or on the host of the pathogen, relative to a host lacking the transformed plant cell.

21. The method of claim **20**, wherein the pathogen exhibits decreased growth following infection of the host plant.

22. The method of claim **20**, wherein the target sequence encodes a protein, the predicted function of which is selected from the group consisting of: ion regulation and transport, enzyme synthesis, nutrient assimilation, viability of the pathogen, sexual reproduction by the pathogen, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, development and differentiation, infection, penetration, development of appressoria or haustoria, mycelial growth, fruiting body growth; sporulation; melanin synthesis, toxin synthesis, siderophore synthesis, sporulation, fruiting body synthesis, cell division, energy metabolism, respiration, cytoskeletal structure synthesis and maintenance, nucleotide metabolism, nitrogen metabolism, carbon metabolism and apoptosis.

23. The method of claim **20**, wherein said pathogen is selected from the group consisting of biotrophic, necrotrophic, and hemibiotrophic fungi.

24. The method of claim **20**, wherein the polynucleotide functions upon being taken up by the pathogen to suppress a gene that performs a function essential for pathogen survival or growth, said function being selected from the group consisting of ion regulation and transport, enzyme synthesis, nutrient assimilation, viability of the pathogen, sexual reproduction by the pathogen, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, development and differentiation, infection, penetration, development of appressoria or haustoria, mycelial growth, fruiting body growth; sporulation; melanin synthesis, toxin synthesis, siderophore synthesis, sporulation, fruiting body synthesis, cell division, energy metabolism, respiration, cytoskeletal structure synthesis and maintenance, nucleotide metabolism, nitrogen metabolism, carbon metabolism and apoptosis.

25. A method for improving the yield of a crop produced from a crop plant subjected to fungal or oomycete infection, said method comprising the steps of

a) introducing a polynucleotide according to claim **1** into said crop plant,

b) cultivating the crop plant to allow the expression of said polynucleotide, wherein expression of the polynucleotide inhibits fungal or oomycete infection or growth and loss of yield due to fungal or oomycete infection.

26. The method of claim **25**, wherein expression of the polynucleotide produces an RNA molecule that suppresses at least a first target gene in a fungal or oomycete plant pathogen that has contacted a portion of said crop plant, wherein the target gene performs at least one essential function selected from the group consisting of ion regulation and transport, enzyme synthesis, nutrient assimilation, viability of the pathogen, sexual reproduction by the pathogen, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, development and differentiation, infection, penetration, development of appressoria or haustoria, mycelial growth, fruiting body growth; sporulation; melanin synthesis, toxin synthesis, siderophore synthesis, sporulation, fruiting body synthesis, cell division, energy metabolism, respiration, cytoskeletal structure synthesis and maintenance, nucleotide metabolism, nitrogen metabolism, carbon metabolism and apoptosis.

27. The method of claim **26**, wherein the pathogen is an ascomycete, a basidiomycete, a deuteromycete, or an oomycete.

28. The method of claim **27**, wherein the pathogen is a rust fungus.

29. The method of claim **28**, wherein the rust fungus is *Phakopsora pachyrizi*.

30. A method of producing a commodity product comprising obtaining a plant according to claim **11** or a part thereof, and preparing a commodity product from the plant or part thereof.

31. A method of producing food or feed, comprising obtaining a plant according to claim **11** or a part thereof and preparing food or feed from said plant or part thereof.

32. The method of claim **31**, wherein the food or feed is defined as oil, meal, protein, starch, flour or silage.

33. A method for suppressing expression of a target gene in a fungal or oomycete cell, the method comprising:

(a) transforming a plant cell with a vector comprising a nucleic acid sequence encoding a dsRNA operatively linked to a promoter and a transcription termination sequence;

(b) culturing the transformed plant cell under conditions sufficient to allow for development of a plant cell culture comprising a plurality of transformed plant cells;

(c) selecting for transformed plant cells that have integrated the vector into their genomes;

(d) screening the transformed plant cells for expression of the dsRNA encoded by the vector;

(e) selecting a plant cell that expresses the dsRNA; and

(f) optionally regenerating a plant from the plant cell that expresses the dsRNA; whereby expression of the gene in the plant is sufficient to modulate the expression of a target gene in a fungal or oomycete cell that contacts the transformed plant or plant cell.

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